

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 8, 2002, 22:59:40 ; Search time 33.09 Seconds
(without alignments)
1042.825 Million cell updates/sec

Title: US-09-635-521A-2
Perfect score: 2334
Sequence: 1 MASPSLPGSDCSQIDHSNV.....NSGAKPANSANAEFGFHEV 453

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

7 number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

PIR-68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	473	20.3	424	2 JH0164	neurotensin recept
2	466.5	20.0	418	2 S29506	neurotensin recept
3	419	18.0	416	2 S68822	neurotensin recept
4	303.5	13.0	378	2 T15816	hypothetical prote
5	272.5	11.7	380	2 I38435	angiotensin recept
6	259.5	11.1	441	2 A41591	endothelin recept
7	256.5	11.0	564	2 A38271	serotonin recept
8	252.5	10.8	428	2 S30508	probable G protein
9	250.5	10.7	428	2 A40201	somatostatin recep
10	250.5	10.7	428	2 S30508	somatostatin recep
11	250.5	10.7	428	2 S30508	somatostatin recep
12	249.5	10.7	398	2 T59336	galanin receptor 1
13	249.5	10.7	398	2 T59336	galanin receptor 1
14	249.5	10.7	427	2 S13424	thyrotropin-releas
15	248.5	10.6	477	2 S71323	alpha-1A adreneryl
16	248.5	10.6	426	2 A40440	endothelin 1 and 2
17	247.5	10.6	394	2 J67209	galanin receptor -
18	247.5	10.6	411	2 I56444	thyrotropin-relea
19	246.5	10.6	412	2 S23436	thyrotropin recep
20	245.5	10.5	418	2 A62226	somatostatin recep
21	245.5	10.5	352	2 J60296	thyrotropin releas
22	244	10.5	427	2 A44158	endothelin recept
23	244	10.5	391	2 A41795	somatostatin recep
24	244	10.5	391	2 A41795	somatostatin recep
25	243.5	10.4	393	2 A39297	thyrotropin-releas
26	242.5	10.4	444	2 A42685	cholecystokin re
27	242	10.3	425	2 T15959	hypothetical prote
28	241.5	10.3	380	2 J62338	kappa opioid recep
29	241	10.3	398	2 I56504	mu opioid receptor

30	241	10.3	398	2 I56517	mu opioid receptor
31	240	10.3	348	1 O080	rhodopsin - bovine
32	239.5	10.3	351	2 S29152	rhodopsin - chike
33	239	10.2	392	2 S65693	opioid receptor mu
34	239	10.2	400	2 I56553	mu opiate receptor
35	238.5	10.2	427	2 S50150	gastric CCK-A rece
36	238	10.2	355	2 A42347	opsin, green-sensl
37	238	10.2	387	2 S55550	5-HT4S receptor -
38	238	10.2	406	2 S55549	serotonin 4 recept
39	237.5	10.2	398	2 A57510	mu opioid receptor
40	237.5	10.2	442	1 J01042	endothelin recepto
41	237.5	10.2	466	2 S36794	beta-1-adrenergic
42	237.5	10.2	466	2 S36794	rhodopsin - rat
43	236	10.1	348	1 S51677	beta-2-adrenergic
44	235.5	10.1	418	1 ORHYB2	kappa opioid recep
45	235	10.1	363	2 A55259	somatostatin recep

ALIGNMENTS

RESULT 1	JH0164	neurotensin receptor - rat
C:Species: Rattus norvegicus (Norway rat)	C:Date: 31-Dec-1991	#sequence_revision 31-Dec-1991 #text_change 17-Mar-2000
C:Accession: JH0164	R:Tanaka, K.; Masu, M.; Nakanishi, S.	
A:Title: Structure and functional expression of the cloned rat neurotensin receptor.	A:Reference number: JH0164; MUID:90297956	
A:Accession: JH0164	A:Molecule type: mRNA	
A:Residues: 1-424 <TM>	C:Comment: Neurotensin receptor belongs to the family of G protein-coupled receptor.	
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein	F:144-165/Domain: transmembrane #status predicted <TM2>	
F:144-165/Domain: transmembrane #status predicted <TM3>	F:189-210/Domain: transmembrane #status predicted <TM4>	
F:236-260/Domain: transmembrane #status predicted <TM5>	F:309-330/Domain: transmembrane #status predicted <TM6>	
F:348-372/Domain: transmembrane #status predicted <TM7>	F:38,42/Binding site: carbohydrate (Asn) (covalent) #status predicted	
Query Match	20.3%; Score 473; DB 2; Length 424;	
Best local similarity	30.3%; Pred. No. 1.6e-33;	
Matches 118; Conservative 67; Mismatches 161; Indels 44; Gaps 8;		
OY	30 KITLLIVYLIIIFMGLISATIRYQVLOKKGY--LQKEYVDHNVSLAGSDIIVFLGM 87	
DB	64 KVLVTAIYIALFVGTGVNSVT--AETLARKKSLOSSTVHYHGLSLALSDLLILLAM 121	
OY	88 PMEYSLIWNPLTSSVTLCKLHFLFEACSVATLILVTLSPFRYTAICHPFYKAVS 147	
DB	122 PVELYNTFVHHNPMWAGDACCRCYVFLRDACVATRALNVASISVERVLAICHPFAKTLM 181	
OY	148 GPCOVKLLIGFVWVTSALVALPILFAMGTEPYLVNPSHRGLTCNRSSRRHNEDETSNM 207	
DB	182 SRSRTKKFSAIMLASALAIPLIFTMGLQ-----NRSQDGTI-----PGG 222	
OY	208 SICITNLSRMT---VQSSIFGAFVYIVLVLSVAFMCNMNOVLN--KSQKGSIA---- 258	
DB	223 LVCPPIVDATFVIVQVNTFMSFLPMLVISTLNTVIANKLIVMVAHQAAEGRGCTVGT 282	
OY	259 -GGRPPQLKSSSEESRTARQTIIFRLIVTVTLAVCMPPQRIKIMAAKPKDWTRES 317	
DB	283 HNGLEHSTFNWLTIEPGVQLLRIGCVLVAIVAVVCCMLPHVRYRLMPCYISDQWTF 342	
OY	318 YFRAYMILPFSETFYLLSSVINPDLTYVSSQOFRRVFGVQLCCRLSDHANHEKRLRVH 377	

Db 343 LDFEYHYFWLTFNALFYSSALIPILYNLSANFRVFLSTLACLCPRHRRKR----- 398
 QY 378 AHSTDSARFVQPLLFASHROSSARFTEK 407
 Db 399 -----PTFSRRKPNSSNHAFTSATRE 421

RESULT 2

S29506
 neurotensin receptor - human
 C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-2000
 C:Accession: S29506
 R:Vita, N.; Laurent, P.; Lefort, S.; Chalou, P.; Dumont, X.; Kaghad, M.; Gully, D.; Le F.
 FEBS Lett. 317, 139-142, 1993
 A:Title: Cloning and expression of a complementary DNA encoding a high affinity human ne
 A:Reference number: S29506; MUID:93154505
 A:Accession: S29506
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-418 <VIT>
 A:Cross-references: EMBL:X70070; NID:g35020; PIDN:CAA49675.1; PID:g35021
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 20.0%; Score 466.5; DB 2; Length 418;
 Best Local Similarity 32.4%; Pred. No. 5.7e-33;
 Matches 114; Conservative 66; Mismatches 137; Indels 35; Gaps 10;

QY 22 EEVAT-WIKITLLVLIIFVGLGNSATIRYQVLOKKGY--LQKEVDHNVSLAC 77
 Db 53 ELVDVTDIYSKVLTAVALFVGTG--TVTAFLARKKSLQSLQSYHYHGLAL 110
 QY 78 SDIIVFLIGMPHEFSITNPLTTSYSLKHLTFLEACSYATLLHVLTSFERYAI 137
 Db 111 SDLLTLLAMPVELNFTVHHMPAFGAGCGRYFLDACTYATLAVASISVERYTAI 170
 QY 138 CHPRFKYKASGFCQYKLLIGFVWTSALVALPLLFAMGTEPLVNVPSHGLTCNRSSTR 197
 Db 171 CHPRFKAATLMSRSRKRKFTSAIWLASALLTYPMLFTMGEO-----NRSDG 216
 QY 198 HHEQETNSMCT---NLSSRWYFQSSIFGAFVYVLLVLSAFCMMQVMQYLR--S 252
 Db 217 QH---AGGLVCPPTITATVAVKVIQVNTFMSFFPMVVISVNTITANKLTVMVROAA 271
 QY 253 QKGL-AGGTRPPQLRKSESESR-ARRQTIIFLRIVTLAVCMMPNRIIRIMAAR 309
 Db 272 EGGQCTVGGGH--STFMALEPRGVQALRGVRLRAVVAIVYVCMPLFHVHRLMFCYI 329
 QY 310 PKHDWTRSYFRAYMILLPESEFFYSSVINPLLYVSSQGFRRVYQVLLCC 361
 Db 330 SDEQWTPFLYDFHYFYWVTFNALFYVSSINPILYNLSANFRHILATLAC 381

RESULT 3

S68822
 neurotensin receptor 2, levocabastine-sensitive - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 20-Jun-2000
 C:Accession: S68822
 R:Chalon, P.; Vita, N.; Kaghad, M.; Guillemot, M.; Bonnin, J.; Delpech, B.; Le Fur, G.;
 FEBS Lett. 386, 91-94, 1996
 A:Title: Molecular cloning of a levocabastine-sensitive neurotensin binding site.
 A:Reference number: S68822; MUID:96228041
 A:Accession: S68822
 A:Molecule type: mRNA
 A:Residues: 1-416 <CHA>
 A:Cross-references: GB:X97121; NID:g1483579; PIDN:CAA65787.1; PID:g1483580
 A:Experimental source: hypothalamus
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

F:33-58/Domain: transmembrane #status predicted <TM1>
 F:70-91/Domain: transmembrane #status predicted <TM2>
 F:110-131/Domain: transmembrane #status predicted <TM3>
 F:155-175/Domain: transmembrane #status predicted <TM4>
 F:204-230/Domain: transmembrane #status predicted <TM5>
 F:296-315/Domain: transmembrane #status predicted <TM6>
 F:335-361/Domain: transmembrane #status predicted <TM7>

Query Match 18.0%; Score 419; DB 2; Length 416;
 Best Local Similarity 28.0%; Pred. No. 7.8e-29;
 Matches 104; Conservative 73; Mismatches 145; Indels 50; Gaps 8;

QY 28 WIKITLLVLIIFVGLGNSATIRYQVLOKKGYLQKEVDHNVSLACSDIIVFLIG 87
 Db 30 WAKVLTALYSLIFAFGAGNALSVM--VLRKAGRGRRLRVHLSIALSALLLVSM 87
 QY 88 PMEYSITNPLTTSYSLKHLTFLEACSYATLLHVLTSFERYAIHPRKAYS 147
 Db 88 PMELYNFWSHYPMVFGDLCRGYFVRELCAVATVLSVLSNERCLAQCPURARLL 147
 QY 148 GPCQVKLLIGFVWTSALVALPLLFAMGTEPLVNVPSHGLTCNRSSTRHNOPTSNM 207
 Db 148 TPRRTRLSLVWVASIGLALPMVAVMGKH---EVESADG-----EPEPAS- 191
 QY 208 SICNLSRWY---FQSSIFGAFVYVLLVLSAFCMMQVMQYLR----- 249
 Db 192 RVCTVLVSRAVLQVFIQVNVLSFALPLATLAFNLGTVHMLALYQVPSASQVSSIP 251
 QY 250 ---MKSQK-----SLAGTRPPQLRKSESESRPARQRTIIFLRIVTLAVCW 296
 Db 252 SRLLESEEGILGTRKTLISGQASLYRHHDAQIRSLQSAQV-LRAIYAVVICH 310
 QY 297 MPNDIRIMAAKPKHDWTRSYFRAYMILLPESEFFYSSVINPLLYVSSQGFRRV 356
 Db 311 LPYARRLMICYIPDDGEMELDYDFHYFYWVNTLFFYSSAVTPILYNAVSSFFKFL 370
 QY 357 QVLCRLSLQHA 368
 Db 371 ESLSGSGEGHS 382

RESULT 4

T15816
 hypothetical protein C48C5.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Mar-2000
 R:Favell, A.
 submitted to the EMBL Data Library, November 1995
 A:Description: The sequence of C. elegans cosmid C48C5.
 A:Reference number: T15816
 A:Accession: T15816
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-378 <FAV>
 A:Cross-references: EMBL:U39994; NID:g1055102; PID:g1055105; PIDN:AAB37017.1; GSPDB:C
 A:Experimental source: strain Bristol N2; clone C48C5
 C:Genetics:
 A:Gene: C48C5.1
 A:Map position: X
 A:Introns: 53/3; 87/2; 136/2; 169/3; 209/3; 231/3; 259/3; 286/1; 327/1
 C:Superfamily: adenosine receptor A1

Query Match 13.0%; Score 303.5; DB 2; Length 378;
 Best Local Similarity 26.2%; Pred. No. 8.2e-19;
 Matches 92; Conservative 66; Mismatches 140; Indels 53; Gaps 14;

QY 27 TWIKITLLVLIIFVGLGNSATIRYQVLOKKGYLQKEVDHNVSLACSDIIVFLIG 86
 Db 50 TLAKYAL--YIFLVGVIGNTT---CLVKKRHPMKTRASMTLMLAVASDLVTLVCG 104

QY 87 MPMEFYSLINMPDLTSSVTLTSCRLHTEFLFECASVATLILVTLTSEFRIALICHF-PHYKA 145
Db 105 LPFE-VVMNNMNOYMPDPEDDYICNLKALIAETTSVSITLITLIERVAACHPLFLMKV 163
QY 146 VSGQCVKLLIGFVWVSALVALPLFLFAMGTEYLVNVPSHRGTLGNSSRTHHEQETS 205
Db 164 QPFRNIGITIGFWMISILCAMFPAIHHRADYIMKMPG-----TDNRIPVK-----SS 213
QY 206 NMSICT-----NLSRMTV--FOSSIFAFVYLVVLVSFAFCMNMNOYLKMSQKSL 257
Db 214 KCMIAVAFEEPKLSTFELFHFSAIAFFALPFTIVILYARIG-----KVSS 262
QY 258 AGGRPPQLKSESEESTARQTIIFRLIVYVLAVOVMNOIRIRMAAKPKH---DW 314
Db 263 NRTTGGELDTTEELQMRIN-----AICATVSAFICYLPQLORLLEFFTDNEVILTW 317
R 5
138435
angiotensin receptor homolog APJ - human
C:Species: Homo sapiens (man)
C:Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 21-Jul-2000
C:Accession: I38435
R:O'Dowd, B.F.; Heiber, M.; Chan, A.; Heng, H.H.; Tsui, L.; Kennedy, J.L.; Shi, X.; Petrucci, D.J.
A:Title: A human gene that shows identity with the gene encoding the angiotensin receptor
A:Reference number: I38435; MUID:94124031
A:Accession: I38435
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-380 <RES>
A:Cross-references: EMBL:U03642; NID:9425351; PIDN:AAA18954.1; PID:9425352
C:Genetics:
A:Gene: APJ
A:Map position: 11q12
A:introns: #status absent
C:superfamily: vertebrate rhodopsin

[illegible]

Db 279 FYFCLPLATLALFTYLTMTCEMLRKKSGM-----OIALNDHUKOREVAKTVECL--V 328
 QY 290 VYLAVQWMMNOIRIRIM-AAAKPKHMDTRSYFRAYMILLPF-SETFEYSSVINPLLYTYS 347
 Db 329 LVFALCWLPHLSRIKLTLTYDDHDPDRCEFLSEFLVLDYIGINNASLNSCINPLALYLV 388
 QY 348 SQQFRFVVOVLCC 361
 Db 389 SKRFKNCFKSCLOC 402

RESULT 7

A38271
 Serotonin receptor 7 - fruit fly (*Drosophila melanogaster*)
 N:Alternate names: 5-hydroxytryptamine receptor 7 (5-HT7)
 C:Species: *Drosophila melanogaster*
 C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 04-Sep-1998
 C:Accession: A38271
 R:Cross: P.; Amlaiky, N.; Plassat, J.L.; Maroteaux, L.; Borrelli, E.; Hen, R.
 Proc. Natl. Acad. Sci. U.S.A. 87, 8940-8944, 1990
 A>Title: Cloning and characterization of a *Drosophila* serotonin receptor that activates
 A:Reference number: A38271; MUID:91062395
 A:Accession: A38271
 A:Molecule type: mRNA
 A:Residues: 1-564 <WIT>
 A:Cross-references: GB:M55533
 A:Note: the authors translated the codon CWT for residue 213 as Ala, GTG for residue 215
 C:Genetics:
 A:Gene: FlyBase:5-HT7
 A:Cross-references: FlyBase:FBgn0004573
 C:Superfamily: octopamine receptor type I
 C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein; phosphoprotein

Query Match 11.1%; Score 259.5; DB 2; Length 564;
 Best Local Similarity 21.1%; Pred. No. 9e-15;
 Matches 92; Conservative 76; Mismatches 145; Indels 123; Gaps 14;

QY 6 LPGSDSQIIDSHVPEFEVATWIKITLLIVLLIFVWGLGNSATIRVTVLQKKGYQ 65
 Db 138 VPLSDPRLLEERFAGEFVRLPLTSIFSVILVILGTVGVVLCVAVCRK---LR 194
 QY 66 KEVTDHNSIACSDILVFLGMPF-EYSLT--WN--PLTTSYTSCKLHFLFEACSY 120
 Db 195 RPNVYLVSLALSDLCVALLVMPALLVELEKMGFPL-----CDIWSFDVLCCT 247
 QY 121 ATLLHVLTSFEERYVIAICHPFRYKAVSGPOVLLIGFVWVSATVALLPLLFAMGTEYPL 180
 Db 248 ASILNCAISVDRLIATYKPLEYGVKRTPRRMVLCVGIWLAACISLEPLLIGNE--- 304
 QY 181 VNPVSHRGILCNRSSTRHNEQPEPTSNMSICTNLSSRWTFVQSSIFGAFVYVLLVSAF 240
 Db 305 -----HDEEGQPICTVOQNF--YQYI--ATLGSFIPILSVMLFYVY 343
 QY 241 MCNNMQVLMSK-----GSLAGSTRPPLKSKSESRARROTI----- 283
 Db 344 QIFRAARRIVLEERKRAQTHLQALNGTSPSAPQAPP-LGHTELASSGNGORSSVGNYS 402
 QY 284 -----FLRLIYVT 291
 Db 403 LTVSTGGGLSSGGGALAGHSGGVSSTGLGSPHHKRLROLAKEKASTLLGIMISA 462
 QY 292 LAVCMNPQIRIRIAAARPKHMDTRSYFRAYMILLPFSETFE---YLSVINPLLYTYS 348
 Db 463 FYVQWLP---FTLLALRP-----FEIMHVPASLSFLMLGIVANSLNIITVATLN 511
 QY 349 QQFRFVVOVLCCRLS 364
 Db 512 RDRFRKPFQDILYFRCS 527

RESULT 8

157940
 Somatostatin receptor 5 - rat
 N:Alternate names: somatostatin release-inhibiting factor subtype 28 receptor
 C:Species: *Rattus norvegicus* (Norway rat)
 C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 24-Nov-1999
 C:Accession: 157940; 157949; S39244
 R:Cross: R.O.; Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.
 Mol. Pharmacol. 44, 1278, 1993
 A>Title: Molecular cloning and expression of a pituitary somatostatin receptor with p
 A:Reference number: 157940; MUID:93125499
 A:Accession: 157940
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-363 <OCA1>
 A:Cross-references: GB:I04535; NID:g455947; PIDN:AA29371.1; PID:g455948
 R:Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.
 Mol. Pharmacol. 44, 1278, 1993
 A>Title: Molecular cloning and expression of a pituitary somatostatin receptor with p
 A:Reference number: 157940; MUID:94088493
 A:Accession: 157949
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 341-363 <OCA2>
 A:Cross-references: GB:S67370; NID:g455947; PIDN:AA29371.1; PID:g455948
 A:Experimental source: pituitary
 R:Penetta, R.; Greenwood, M.; Patel, Y.C.
 submitted to the EMBL Data Library, August 1993
 A:Description: Correction of the nucleotide and amino acid sequence of the rat somato
 A:Reference number: S39244
 A:Accession: S39244
 A:Molecule type: mRNA
 A:Residues: 309-363 <PEN>
 A:Cross-references: EMBL:X74828; NID:g433911; PIDN:CAA52825.1; PID:g433912
 C:Genetics:
 A:Gene: SSTR5
 C:Superfamily: vertebrate rhodopsin

Query Match 11.0%; Score 256.5; DB 2; Length 363;
 Best Local Similarity 28.2%; Pred. No. 9.9e-13;
 Matches 98; Conservative 54; Mismatches 109; Indels 87; Gaps 18;

QY 35 LVYLIIFWGLGNSATIRVTVLQKKGYLDQEVYD-HVMSIACSDILVFLGMPMEFYS 93
 Db 42 VYLVLTCTVGLSGNTLVYVLRNAK---KTYTNYIILAAVDYL-FMLGILP----- 92
 QY 94 IIVNPLTTSYTL-----CKLHFLFACGSYATLLHVLTSFEERYVIAICHPFRYKA 145
 Db 93 -----LATQNVVSYWPGSFLCRLVMTLDGINQFTSIFCLMWSVDYRLAVHPLRSAR 147
 QY 146 VSGPCVKILIGFVWVSATVALLPLLFAMGTEYPLVNPVSHRGILCNRSSTRHNEQPEPT 205
 Db 148 WRRPRVAKMASAAVWVFLMSLPLV-----FADQDEGWS--TCNLS-----WPEPV 193
 QY 206 NMSICTNLSSRWTFVQSSIFGAFVYVLL-----LSVAFCMNNMQVLMSKQSGSLAG 260
 Db 194 GL-----WG-----AAFTYTSVLGFGFGLVLYICLYLIVYK-----AAG 231
 QY 261 TRPPLKSKSESESTRARQTIIFRLIYVTLAV---CWNQDRIIRI--MAAKPKHMDT 315
 Db 233 MRVGSRRRRSEPKYT-----RMVVVVVIVFGVGMLEPFIVNLVNLAFLEPPEPTS 282
 QY 316 RS-YFRAYMILLPFSETFYSSVINPLLYVSSQOFRFVVOVLCCR 362
 Db 283 AGLYF--FVVVLS-----YANSCANPLLYGFLSDNFRQSPKRYLCUR 322

RESULT 9

330508
 probable G protein-coupled receptor - rat
 C:Species: *Rattus norvegicus* (Norway rat)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jan-2000
 C:Accession: S30508

R: Meyerhof, W.; Wulfsen, I.; Schoenrock, C.; Fehr, S.; Richter, D.

Proc. Natl. Acad. Sci. U.S.A. 89, 10267-10271, 1992

A: Title: Molecular cloning of a somatostatin-28 receptor and comparison of its expression

A: Reference number: S30508; MUID:93066220

A: Accession: S30508

A: Status: preliminary

A: Molecule type: mRNA

A: Residues: 1-428 <MEY>

A: Cross-references: EMBL:X63574; NID:956315; PIDN:CAA5130.1; PID:956316

A: Note: Sequence extracted from NCBI database (NCBI:115746)

C: Superfamily: vertebrate rhodopsin

C: Keywords: G protein-coupled receptor; transmembrane protein

Query Match 10.8%; Score 252.5; DB 2; Length 428;

Best Local Similarity 26.5%; Pred. No. 2.7e-14;

Matches 90; Conservative 69; Mismatches 123; Indels 57; Gaps 16;

31 ITLLIVYLIIIFMGILGNSATIRVYLOKKGYLQKEVTD-HMVSACSDILVFLIGMPM 89

46 ILISLVIVLVVGVGLGNSLVITY--VLRHNS--SPSVTSYIILNLADEL-FMLGLP- 99

90 EYSLINPLTSSV-TLSCKLHFLFEACSYATLLVTLSEFERYTAICHPERYKAVSG 148

100 --FLAQAQALSYFPGSLMCRVMAVVDGINGFTSIFCLVMSVDRLAVVHPTRSARMT 157

149 PCQYKALIGFWVWTSALVALPLFAMGTEFLVWVPSHRLGTCNRSSTRIHDEPETSMS 208

158 APVARMVSAVAWVASAVVLPVVFSG-----VP--RGM-----STCHQWDEP----- 199

209 ICTNLSSRWTFQSSIFGAFVYLVV-----LSVAFMCMNMVLMKSQKSLAGSTRP 263

200 -----AAAWRT-----AFIITVALGFEPLVLYICLILYVVKRSTTRV-----RA 243

264 POLRKESESESRARQTIIFRLIVYTLA--VCMPNQRIRMAAARPKHDMTRSYFR 320

244 PSCQWQAPACQRRRRSRRTVMVAVALFVLCWMPFYLINIVVCPLE-EPAFFG 302

321 AYMLLPSETFEFLSSVINPLTYVSSQOFRRVFOYL 359

303 LYFLVVALP---YANSCANPILYGLFSTRFKQGFRRIL 337

RESULT 10

A44021

Somatostatin receptor SSTR3 - mouse

C: Species: Mus musculus (house mouse)

C: Date: 10-Jun-1993 #sequence, revision 18-Nov-1994 #text, change 11-Jan-2000

C: Accession: A44021

R: Gauda, K.; Rens-Domiano, S.; Breder, C.D.; Law, S.F.; Saper, C.B.; Reisine, T.; Bell,

J. Biol. Chem. 267, 20422-20428, 1992

A: Title: Cloning of a novel somatostatin receptor, SSTR3, coupled to adenylyl cyclase.

A: Reference number: A44021; MUID:93015924

A: Accession: A44021

A: Status: preliminary; not compared with conceptual translation

A: Molecule type: nucleic acid

A: Residues: 1-428 <YAS>

A: Cross-references: GB:M91000; NID:9201065; PIDN:AAA40144.1; PID:9201066

A: Note: Sequence extracted from NCBI database (NCBI:115746)

C: Superfamily: vertebrate rhodopsin

C: Keywords: G protein-coupled receptor; transmembrane protein

Query Match 10.7%; Score 250.5; DB 2; Length 428;

Best Local Similarity 26.5%; Pred. No. 4e-14;

Matches 90; Conservative 69; Mismatches 123; Indels 57; Gaps 16;

31 ITLLIVYLIIIFMGILGNSATIRVYLOKKGYLQKEVTD-HMVSACSDILVFLIGMPM 89

46 ILISLVIVLVVGVGLGNSLVITY--VLRHNS--SPSVTSYIILNLADEL-FMLGLP- 99

90 EYSLINPLTSSV-TLSCKLHFLFEACSYATLLVTLSEFERYTAICHPERYKAVSG 148

100 --FLAQAQALSYFPGSLMCRVMAVVDGINGFTSIFCLVMSVDRLAVVHPTRSARMT 157

149 PCQYKALIGFWVWTSALVALPLFAMGTEFLVWVPSHRLGTCNRSSTRIHDEPETSMS 208

158 APVARMVSAVAWVASAVVLPVVFSG-----VP--RGM-----STCHQWDEP----- 199

209 ICTNLSSRWTFQSSIFGAFVYLVV-----LSVAFMCMNMVLMKSQKSLAGSTRP 263

200 -----AAAWRT-----AFIITVALGFEPLVLYICLILYVVKRSTTRV-----RA 243

264 POLRKESESESRARQTIIFRLIVYTLA--VCMPNQRIRMAAARPKHDMTRSYFR 320

244 PSCQWQAPACQRRRRSRRTVMVAVALFVLCWMPFYLINIVVCPLE-EPAFFG 302

321 AYMLLPSETFEFLSSVINPLTYVSSQOFRRVFOYL 359

303 LYFLVVALP---YANSCANPILYGLFSTRFKQGFRRIL 337

RESULT 11

I59336

galanin receptor 1 - human

C: Species: Homo sapiens (man)

C: Date: 31-May-1996 #sequence, revision 31-May-1996 #text, change 21-Jul-2000

C: Accession: I59336; J05801; G01765; G02528

R: Habert-Ortoli, E.; Amiranoff, B.; Loquet, I.; Laburthe, M.; Mayaux, J.

Proc. Natl. Acad. Sci. U.S.A. 91, 9780-9783, 1994

A: Title: Molecular cloning of a functional human galanin receptor.

A: Reference number: I59336; MUID:95024044

A: Accession: I59336

A: Status: preliminary; translated from GB/EMBL/DBJ

A: Molecule type: mRNA

A: Residues: 1-349 <RAB>

A: Cross-references: GB:I34339; NID:9559047; PIDN:AAA50767.1; PID:9559048

R: Lormier, D.D.; Matkowsky, K.; Benya, R.V.

Biochem. Biophys. Res. Commun. 241, 558-564, 1997

A: Title: Cloning, chromosomal location, and transcriptional regulation of the human 9

A: Reference number: J05801; MUID:98086390

A: Accession: J05801

A: Status: nucleic acid sequence not shown

A: Molecule type: mRNA

A: Residues: 1-349 <LOR>

A: Cross-references: GB:U53511; NID:91297337; PIDN:JACS1936.1; PID:91297338

A: Note: submitted to the EMBL Data Library, April 1996

R: Ross, P.C.

submitted to the EMBL Data Library, March 1995

A: Reference number: G08350

A: Accession: G01765

A: Status: translated from GB/EMBL/DBJ

A: Molecule type: mRNA

A: Residues: 1-14, 'W', 16-349 <ROS>

A: Cross-references: EMBL:U23854; NID:9775209; PID:9775210

C: Comment: This receptor inhibits cAMP formation, stimulates and inhibits phospholipid

, and increases arachidonic acid metabolism, as well as opens ATP-dependent K⁺ but Cl

, Genetics

A: Gene: GDB:GALNR

A: Cross-references: GDB:392699; OMIM:600377

A: Map position: 18q23-18q23

C: Superfamily: vertebrate rhodopsin

Query Match 10.7%; Score 250; DB 2; Length 349;

Best Local Similarity 23.6%; Pred. No. 3.5e-14;

Matches 91; Conservative 64; Mismatches 147; Indels 84; Gaps 16;

21 PEEFVATWIKITLLIVYLIIIFMGILGNSATIRVYLOKKGYLQKEVTDHMSACSDI 80

25 PLRGIGVENFTLV-VGLIFALGVGNSLVITVL-ARSPGKPRSTNLFILNLSIADL 82

81 LVFLIGMPMEYSLINPLTSSVTLSCKLHFLFEACSYATLLVTLSEFERYTAICHP 140

83 AYLLFCIP--FQATVVALPLVWLGAFICKIHFYFTYSMLVSTFILAAMVDVVAIVHS 140

141 FRKAVSGPCQYKALIGFWVWTSALVALPLFAMGTEFLVWVPSHRLGTCNRSSTRHHE 200

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Db 141 KRSSSLKRSNALLGVGCIWALISIMASPVAY-----HGGILF----- 177
QY 201 QPETSINMSTCTLLSSRMT-----VFQSSIFGAFVYVLYLVLSVAMCMNMOMVLKKS 252
Db 178 HPRASNQQFFCW---BQMDPPRRKKAYVCTFVEG---YLLPLLICICCYAKVNLHLKK 230
QY 253 QKSLAGTRPPQLRKSESESRARQTIIFLRLLIYVTLAVCMNPNOIRIRMAAKPKH 312
Db 231 LKN-----MSKSESKSKKKA---QTVL---VVVVVFGISWLPNHH-----IH 267
QY 313 DWTRSYFRAYMLLPSESEF-----FYLSVYPLLYTYSSQDFRFRVVOYLCCRLSL 365
Db 268 LWAE--FGVEP--LTPASFLFRITACLVANSNSVNPDIYAFLESENRKAYKQVFKCH-- 322
QY 366 QHANHEKRLRVHAHSTTDSARFVQRP 391
Db 323 -----RKSHLSPTKKNKSRIDPP 341

Respect 12
JN0708
thyrotropin-releasing hormone receptor - human
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Jun-2000
C:Accession: S40682; JN0759; S50151; S50152; I38356; JN0708
R:Matre, V.; Karlens, H.E.; Wright, M.S.; Lundell, I.; Fjeldheim, A.K.; Gabrielsen, O.S.
Biochem. Biophys. Res. Commun. 195, 179-185, 1993
A:Title: Molecular cloning of a functional human thyrotropin-releasing hormone receptor.
A:Reference number: S40682; MUID:93371401
A:Accession: S40682
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-398 <MAT>
A:Cross-references: EMBL:X75071; NID:q404157; PIDN:CAA52965.1; PID:q404158
R:Tamada, M.; Monden, T.; Satoh, T.; Satoh, N.; Murakami, M.; Iriuchijima, T.; Kakegawa,
Biochem. Biophys. Res. Commun. 195, 737-745, 1993
A:Title: Pituitary adenomas of patients with acromegaly express thyrotropin-releasing hc
prior gene.
A:Reference number: JN0759; MUID:93384596
A:Accession: JN0759
A:Molecule type: mRNA
A:Residues: 1-398 <YAM>
A:Cross-references: GB:D16845; NID:q577631; PIDN:BA04120.1; PID:q577632
R:Hinnema, S.; Hosoya, M.; Ogi, K.; Tanaka, H.; Nagai, Y.; Onda, H.
Biochim. Biophys. Acta 1219, 251-259, 1994
A:Title: Molecular cloning and functional expression of a human thyrotropin-releasing hc
A:Reference number: S50151; MUID:95002135
A:Accession: S50151
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-263 <HIN>
A:Accession: S50152
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 267-398 <H12>
R:Duthie, S.M.; Taylor, P.L.; Anderson, L.; Cook, J.; Eidine, K.A.
Mol. Cell. Endocrinol. 95, R11-R15, 1993
A:Title: Cloning and functional characterisation of the human TRH receptor.
A:Reference number: I38356; MUID:94063224
A:Accession: I38356
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-398 <RES>
A:Cross-references: EMBL:X72089; NID:q440155; PIDN:CAA50979.1; PID:q440156
C:Genetics:
A:Gene: GDB:TRHR
A:Cross-references: GDB:228955; OMIM:188545
A:Map position: 8q23-8q23
C:Superfamily: adenosine receptor A1
C:Keywords: G protein-coupled receptor; receptor; transmembrane protein
F:29-51/Domain: transmembrane #status predicted <TM>
F:62-83/Domain: transmembrane #status predicted <TM2>

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F:101-121/Domain: transmembrane #status predicted <TM3>
F:146-168/Domain: transmembrane #status predicted <TM4>
F:194-215/Domain: transmembrane #status predicted <TM5>
F:267-288/Domain: transmembrane #status predicted <TM6>
F:297-319/Domain: transmembrane #status predicted <TM7>

Query Match 10.7%; Score 249.5; DB 2; Length 398;
Best Local Similarity 22.0%; Pred. No. 4, 9e-14;
Matches 86; Conservative 69; Mismatches 119; Indels 117; Gaps 12;

QY 21 PEFVATWIKITLLVLYLIFVWGLGNSATIRVTOYLOKGYLOKEVTDHMYSLACSDI 80
Db 16 PRAVVALEYQVITLLVLLICGLGIVGN---IMVLYVMTKTHMRPTNCTYLSLAVADL 72
QY 81 LVFL-IGMPMEFYSIINNPPLTSSY-----TLCKLHTEFLFACSVATLLHVLTSFER 133
Db 73 MVLVAAGP-----NITDSIYGSWYGYVGCITLYLOYLGINASSCSITAFIER 123
QY 134 YIAICHPFRKAVSGPCQVKLLIGFVWTSALVALPLLFMGTEYPLVNPFSHRC---LT 190
Db 124 YIAICHPKAKQFLCTFESRAKILIFVWAFSLCYMLWFLLD-----LNTSTYKDAIVIS 178
QY 191 CNRSTRRHDEPETSINMSTCTNLSRMTVFQSSIFGAFVYVLYLVLSVAPCMNMOMQVLM 250
Db 179 CGYKISRWTYSP-----IYLMDFGVYVVPMLAIVLV----- 211
QY 251 KSKQSLAGTRPPQLRKSESESR-----ARQTIIF 284
Db 212 -----GFIARILFLNPIDSPDENSKTWKNDSTHQNTMLNVNTSNRCFNSVSSRKQYTKM 267
QY 285 LRLVYVTLAVCMNPNOIRIRMAAKPKHDWTRSFRAVYML-----LPSESEF----- 333
Db 268 LAVVYVIFALMLP-----YRLVAVNSFLSPFQENWPLFCRI 307
QY 334 --YLSVYINPLLYTYSSQDFRFRVVOYLCCR 362
Db 308 CTVLSAINPVITVIMLSQKFAFRKILCNCK 338

RESULT 13
S13424
endothelin receptor - bovine
C:Species: Bos primigenius laurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
C:Accession: S13424
R:Araki, H.; Hori, S.; Aramori, I.; Ohkubo, H.; Nakanishi, S.
Nature 348, 730-732, 1990
A:Title: Cloning and expression of a cDNA encoding an endothelin receptor.
A:Reference number: S13424; MUID:91080923
A:Accession: S13424
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-427 <ARA>
A:Cross-references: GB:X57765; NID:q121; PIDN:CAA40917.1; PID:q122
C:Superfamily: endothelin receptor B

Query Match 10.7%; Score 249.5; DB 2; Length 427;
Best Local Similarity 23.2%; Pred. No. 4, 9e-14;
Matches 92; Conservative 84; Mismatches 152; Indels 69; Gaps 19;

QY 17 HSHVP-EFEVATWIKITLLVLYLIFVWGLGNSATIRVTOYLOKGYLOKEVTDHMYSL 75
Db 66 HNYCQOQKRIKISAFKYNITVISTCTFIYGVGNMTLLRI--IYQNK-CMRGPNALIASL 122
QY 76 ACSDLVFLKIGMPMEFYSIT--WNPLTSSY--TLCKLHTEFLFACSVATLLHVLTSF 131
Db 123 ALGDLIYVYIDLPIVWFKLLAGRW--PEQNDPFGVFLCKLFPFLKSSVGTIVMLCALSV 181
QY 132 ERYIAICHPFRKAVSGPCQVKLLIGFVWTSALVALPLLFMGTEYPLVNP-----S 185
Db 182 DTRAVASMSRVOGIGIPLVYIAIVLSIWLIFLAIIP--EATG-----FVWVPEYKGAQ 235

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